

WYS-018.04 -- SEQLIST.TXT
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Freeman, Gordon J.
Nadler, Lee M.
Gray, Gary S.

(ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 WITH INCREASED IMMUNOGENICITY AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley Hoag
(B) STREET: 155 Seaport Boulevard
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10/767,561
(B) FILING DATE: 28-JAN-2004
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/101,624;
(B) FILING DATE: 26-JUL-1993;
(A) APPLICATION NUMBER: 08/109,393;
(B) FILING DATE: 19-AUG-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Russell, Hathaway P.
(B) REGISTRATION NUMBER: 46,488
(C) REFERENCE/DOCKET NUMBER: WYS-018.04

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 832-1000
(B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
GAGTGGGGTC ATTTCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC	115
Met Asp Pro	1
CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	5 10 15
CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	20 25 30 35
GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	40 45 50
GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	55 60 65
GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355
Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	70 75 80
GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
Gly Arg Thr Asn Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	85 90 95
CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451
Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	100 105 110 115
AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499
Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	120 125 130
GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	547
Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Thr Asn Ile	135 140 145
ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	150 155 160
CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643
Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	165 170 175
ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA	691
Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	180 185 190 195
CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG	739
Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	200 205 210

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AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu	787
215 TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro	835
230 GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	883
245 GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Trp Lys Lys Lys Arg	931
260 CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu	979
280 AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser	1027
295 GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp	1075
310 AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA Lys Ser Asp Thr Cys Phe	1120
325	

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met 1 5 10 15
Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe 20 25 30
Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln 35 40 45
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val 50 55 60
Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser 65 70 75 80
Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg 85 90 95

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Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
 100 105 110
 His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
 115 120 125
 Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
 130 135 140
 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
 145 150 155 160
 His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
 165 170 175
 Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
 180 185 190
 Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
 195 200 205
 Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
 210 215 220
 Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
 225 230 235 240
 Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
 245 250 255
 Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
 260 265 270
 Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
 275 280 285
 Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
 290 295 300
 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
 305 310 315 320
 Ser Cys Asp Lys Ser Asp Thr Cys Phe
 325

(4) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 99..1028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT

60

CCTGTAGACG TGTTCAGAA CTTACGGAAG CACCCACG ATG GAC
Met Asp

104

1

CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG
Pro Arg Cys 5 Thr Met Gly Leu Ala 10 Ile Leu Ile Phe Val 15 Thr Val Leu

152

CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG
Leu Ile 20 Ser Asp Ala Val Ser 25 Val Glu Thr Gln Ala 30 Tyr Phe Asn Gly

200

ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG
Thr 35 Ala Tyr Leu Pro 40 Pro Phe Thr Lys 45 Gln Asn Ile Ser Leu 50

248

AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC
Ser Glu Leu Val 55 Phe Trp Gln Asp 60 Gln Lys Leu Val 65 Leu Tyr

296

GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC
Glu His Tyr Leu 70 Gly Thr Glu Lys 75 Leu Asp Ser Val Asn Ala 80 Lys Tyr

342

CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC
Leu Gly Arg 85 Thr Ser Phe Asp Arg 90 Asn Asn Trp Thr Leu Arg 95 Leu His

382

AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA
Asn Val 100 Gln Ile Lys Asp Met 105 Gly Ser Tyr Asp Cys 110 Phe Ile Gln Lys

440

AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG
Lys 115 Pro Pro Thr Gly Ser 120 Ile Ile Leu Gln 125 Thr Leu Thr Glu Leu 130

488

TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT
Ser Val Ile Ala Asn 135 Phe Ser Glu Pro 140 Ile Lys Leu Ala 145 Gln Asn

536

GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT
Val Thr Gly Asn 150 Ser Gly Ile Asn 155 Thr Thr Cys Thr Ser Lys 160 Gln Gly

584

CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT
His Pro Lys 165 Pro Lys Met Tyr 170 Phe Leu Ile Thr Asn Ser Thr Asn

632

GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG
Glu Tyr 180 Gly Asp Asn Met 185 Gln Ile Ser Gln 190 Asn Val Thr Glu Leu

680

TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG
Phe Ser Ile Ser Asn 200 Ser Leu Ser Leu Ser 205 Pro Asp Gly Val 210 Trp

728

CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC
His Met Thr Val 215 Val Cys Val Leu Glu Thr 220 Glu Ser Met Lys 225 Ile Ser

776

TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT
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Ser	Lys	Pro	Leu	Asn	Phe	Thr	Gln	Glu	Phe	Pro	Ser	Pro	Gln	Thr	Tyr		
			230					235					240				
TGG	AAG	GAG	ATT	ACA	GCT	TCA	GTT	ACT	GTG	GCC	CTC	CTC	CTT	GTG	ATG		872
Trp	Lys	Glu	Ile	Thr	Ala	Ser	Val	Thr	Val	Ala	Leu	Leu	Leu	Val	Met		
		245					250				255						
CTG	CTC	ATC	ATT	GTA	TGT	CAC	AAG	AAG	CCG	AAT	CAG	CCT	AGC	AGG	CCC		920
Leu	Leu	Ile	Ile	Val	Cys	His	Lys	Lys	Pro	Asn	Gln	Pro	Ser	Arg	Pro		
		260				265					270						
AGC	AAC	ACA	GCC	TCT	AAG	TTA	GAG	CGG	GAT	AGT	AAC	GCT	GAC	AGA	GAG		968
Ser	Asn	Thr	Ala	Ser	Lys	Leu	Glu	Arg	Asp	Ser	Asn	Ala	Asp	Arg	Glu		
275					280				285						290		
ACT	ATC	AAC	CTG	AAG	GAA	CTT	GAA	CCC	CAA	ATT	GCT	TCA	GCA	AAA	CCA		1016
Thr	Ile	Asn	Leu	Lys	Glu	Leu	Glu	Pro	Gln	Ile	Ala	Ser	Ala	Lys	Pro		
			295					300						305			
AAT	GCA	GAG	TGAAGGCAGT	GAGAGCCTGA	GGAAAGAGTT	AAAAATTGCT											1065
Asn	Ala	Glu															
TTGCCTGAAA	TAAGAAGTGC	AGAGTTTCTC	AGAATTCAAA	AATGTTCTCA	GCTGATTGGA												1115
ATTCTACAGT	TGAATAATTA	AAGAAC															1151

(5) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Pro	Arg	Cys	Thr	Met	Gly	Leu	Ala	Ile	Leu	Ile	Phe	Val	Thr		
1				5				10					15				
Val	Leu	Leu	Ile	Ser	Asp	Ala	Val	Ser	Val	Glu	Thr	Gln	Ala	Tyr	Phe		
			20					25					30				
Asn	Gly	Thr	Ala	Tyr	Leu	Pro	Cys	Pro	Phe	Thr	Lys	Ala	Gln	Asn	Ile		
			35				40					45					
Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Gln	Lys	Leu	Val		
			50			55				60							
Leu	Tyr	Glu	His	Tyr	Leu	Gly	Thr	Glu	Lys	Leu	Asp	Ser	Val	Asn	Ala		
65				70				75						80			
Lys	Tyr	Leu	Gly	Arg	Thr	Ser	Phe	Asp	Arg	Asn	Trp	Thr	Leu	Arg			
			85					90					95				
Leu	His	Asn	Val	Gln	Ile	Lys	Asp	Met	Gly	Ser	Tyr	Asp	Cys	Phe	Ile		
			100					105					110				
Gln	Lys	Lys	Pro	Pro	Thr	Gly	Ser	Ile	Ile	Leu	Gln	Gln	Thr	Leu	Thr		
		115				120						125					

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Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala
 130 135 140
 Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys
 145 150 155 160
 Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser
 165 170 175
 Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
 180 185 190
 Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly
 195 200 205
 Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys
 210 215 220
 Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln
 225 230 235 240
 Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu
 245 250 255
 Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser
 260 265 270
 Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
 275 280 285
 Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
 290 295 300
 Lys Pro Asn Ala Glu
 305

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60
 GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCTC TCAGCAAGCT 120
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GTGAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT	180
GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTATCATCAGC CCTGCCTGTT	240
TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGGCTTT CACTTTTGAC	300
CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC	353
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser	
-30 -25	
AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT	401
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu	
-20 -15 -10	
TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA	449
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu	
-5 1 5	
GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA	497
Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala	
15 20 25	
CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG	545
Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met	
30 35 40	
ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC	593
Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile	
45 50 55	
TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA	641
Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro	
60 65 70	
TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC	689
Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp	
75 80 85 90	
GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT	737
Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala	
95 100 105	
GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT	785
Asp Phe Pro Thr Ile Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn	
110 115 120	
ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC	833
Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His	
125 130 135	
CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA	881

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Leu	Ser	Trp	Leu	Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr		
140						145					150						

GTT	TCC	CAA	GAT	CCT	GAA	ACT	GAG	CTC	TAT	GCT	GTT	AGC	AGC	AAA	CTG	929	
Val	Ser	Gln	Asp	Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu		
155					160					165					170		

GAT	TTC	AAT	ATG	ACA	ACC	AAC	CAC	AGC	TTC	ATG	TGT	CTC	ATC	AAG	TAT	977	
Asp	Phe	Asn	Met	Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr		
				175					180					185			

GGA	CAT	TTA	AGA	GTG	AAT	CAG	ACC	TTC	AAC	TGG	AAT	ACA	ACC	AAG	CAA	1025	
Gly	His	Leu	Arg	Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln		
			190					195					200				

GAG	CAT	TTT	CCT	GAT	AAC	CTG	CTC	CCA	TCC	TGG	GCC	ATT	ACC	TTA	ATC	1073	
Glu	His	Phe	Pro	Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	Ile		
		205					210					215					

TCA	GTA	AAT	GGA	ATT	TTT	GTG	ATA	TGC	TGC	CTG	ACC	TAC	TGC	TTT	GCC	1121	
Ser	Val	Asn	Gly	Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	Ala		
	220					225					230						

CCA	AGA	TGC	AGA	GAG	AGA	AGG	AGG	AAT	GAG	AGA	TTG	AGA	AGG	GAA	AGT	1169	
Pro	Arg	Cys	Arg	Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu	Ser		
235				240					245						250		

GTA	CGC	CCT	GTA	TAACAGTGT	CGCAGAA	GCA	AGGGCTGAA	AAGATCTGAA	1221								
Val	Arg	Pro	Val														

GGTAGCCTCC	GTCACTCTCT	CTGGGATACA	TGGATCGTGG	GGATCATGAG	GCATTCCTCC	1281											
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CTTAACAAAT	TTAAGCTGTT	TTACCCACTA	CCTCACCTTC	TTAAAAACCT	CTTTCAGATT	1341											
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AAGCTGAACA	GTTACAAGAT	GGCTGGCATC	CCTCTCCTTT	CTCCCCATAT	GCAATTTGCT	1401											
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TAATGTAACC	TCTTCTTTTG	CCATGTTTCC	ATTCTGCCAT	CTTGAATTGT	CTTGTCAGCC	1461											
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AATTCATTAT	CTATTAAACA	CTAATTTGAG	1491														
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(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 -30 -25 -20
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 -15 -10 -5
 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 -1 1 5 10
 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 15 20 25 30
 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 35 40 45
 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 50 55 60
 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 65 70 75
 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 80 85 90
 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 95 100 105 110
 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 115 120 125
 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 130 135 140
 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 145 150 155
 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
 160 165 170
 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
 175 180 185 190

 Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
 195 200 205
 Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
 210 215 220
 Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
 225 230 235
 Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 240 245 250

(8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mus musculus*
 (D) DEVELOPMENTAL STAGE: germ line
 (F) TISSUE TYPE: lymphoid
 (G) CELL TYPE: B lymphocyte
 (H) CELL LINE: 70Z and A20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GAGTTTATA CCTCAATAGA CTCTACTAG TTTCTCTTT TCAGGTTGTG AAACCAACC      60
TTCAAAGACA CTCTGTGCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG    120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA    180
GGTGCCTAAG CTCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT    240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC      290
      Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
      -35                      -30                      -25

AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT      338
Lys Phe Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg
      -20                      -15                      -10

CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG      386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
      -5                      -1      1                      5

AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT      434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
      10                      15                      20                      25

GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG      482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
      30                      35                      40

TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG      530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
      45                      50

ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC      578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
      60                      65                      70

CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA      626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Lys Glu Arg
      75                      80                      85

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GGA Gly	ACG Thr	TAT Tyr	GAA Glu	GTT Val	AAA Lys	CAC His	TTG Leu	GCT Ala	TTA Leu	GTA Val	AAG Lys	TTG Leu	TCC Ser	ATC Ile	AAA Lys	674
90					95					100					105	
GCT Ala	GAC Asp	TTC Phe	TCT Ser	ACC Thr	CCC Pro	AAC Asn	ATA Ile	ACT Thr	GAG Glu	TCT Ser	GGA Gly	AAC Asn	CCA Pro	TCT Ser	GCA Ala	722
				110					115					120		
GAC Asp	ACT Thr	AAA Lys	AGG Arg	ATT Ile	ACC Thr	TGC Cys	TTT Phe	GCT Ala	TCC Ser	GGG Gly	GGT Gly	TTC Phe	CCA Pro	AAG Lys	CCT Pro	770
			125					130					135			
CGC Arg	TTC Phe	TCT Ser	TGG Trp	TTG Leu	GAA Glu	AAT Asn	GGA Gly	AGA Arg	GAA Glu	TTA Leu	CCT Pro	GGC Gly	ATC Ile	AAT Asn	ACG Thr	818
			140				145					150				
ACA Thr	ATT Ile	TCC Ser	CAG Gln	GAT Asp	CCT Pro	GAA Glu	TCT Ser	GAA Glu	TTG Leu	TAC Tyr	ACC Thr	ATT Ile	AGT Ser	AGC Ser	CAA Gln	866
	155					160					165					
CTA Leu	GAT Asp	TTC Phe	AAT Asn	ACG Thr	ACT Thr	CGC Arg	AAC Asn	CAC His	ACC Thr	ATT Ile	AAG Lys	TGT Cys	CTC Leu	ATT Ile	AAA Lys	914
170					175					180					185	
TAT Tyr	GGA Gly	GAT Asp	GCT Ala	CAC His	GTG Val	TCA Ser	GAG Glu	GAC Asp	TTC Phe	ACC Thr	TGG Trp	GAA Glu	AAA Lys	CCC Pro	CCA Pro	962
				190					195					200		
GAA Glu	GAC Asp	CCT Pro	CCT Pro	GAT Asp	AGC Ser	AAG Lys	AAC Asn	ACA Thr	CTT Leu	GTG Val	CTC Leu	TTT Phe	GGG Gly	GCA Ala	GGA Gly	1010
		205						210					215			
TTC Phe	GGC Gly	GCA Ala	GTA Val	ATA Ile	ACA Thr	GTC Val	GTC Val	ATC Ile	GTT Val	GTC Val	ATC Ile	ATC Ile	AAA Lys	TGC Cys		1058
		220				225				230						
TTC Phe	TGT Cys	AAG Lys	CAC His	AGA Arg	AGC Ser	TGT Cys	TTC Phe	AGA Arg	AGA Arg	AAT Asn	GAG Glu	GCA Ala	AGC Ser	AGA Arg	GAA Glu	1106
	235					240					245					
ACA Thr	AAC Asn	AAC Asn	AGC Ser	CTT Leu	ACC Thr	TTC Phe	GGG Gly	CCT Pro	GAA Glu	GAA Glu	GCA Ala	TTA Leu	GCT Ala	GAA Glu	CAG Gln	1154
250					255				260						265	
ACC Thr	GTC Val	TTC Phe	CTT Leu	TAGTCTTCT	CTGTCCATGT	GGGATACATG	GTATTATGTG									1206
GCTCATGAGG	TACAATCTTT	CTTTCAGCAC	CGTGCTAGCT	GATCTTTCGG	ACAACCTTGAC											1266
ACAAGATAGA	GTAACTGGG	AAGAGAAAGC	CTTGAATGAG	GATTTCTTTC	CATCAGGAAG											1326
CTACGGGCAA	GTTTGCTGGG	CCTTTGATTG	CTTGATGACT	GAAGTGGAAG	GGCTGAGCCC											1386
ACTGTGGGTG	GTGCTAGCCC	TGGGCAGGGG	CAGGTGACCC	TGGTGGTAT	AAGAAAAAGA											1446
GCTGTCACTA	AAAGGAGAGG	TGCCTAGTCT	TACTGCAACT	TGATATGTCA	TGTTTGTTG											1506
GTGCTGTGG	GAGGCCTGCC	CTTTTCTGAA	GAGAAGTGGT	GGGAGAGTGG	ATGGGGTGGG											1566
GGCAGAGGAA	AAGTGGGGGA	GAGGGCCTGG	GAGGAGAGGA	GGGAGGGGGA	CGGGGTGGGG											1626

190
Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
205 210 215
Ala Val Ile Thr Val Val Val Ile Val Val Ile Lys Cys Phe Cys
220 225 230 235
Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
240 245 250
Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
255 260 265
Phe Leu

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTTAGAGCACA

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCTAAAG

(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAATACGACTCACTATAGGG

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAAGGTTCTTCACAAAG

(14) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACATAAGCCTGAGTGAGCTGG

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGATGAGCAGCATCACAAGG

(16) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGAGTGAGTCCGAATAC

(17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GACGAGTAGTAACATACAGTG

(18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 111..1040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCACGCGTC CGGAGCAAG CAGACGCGTA AGAGTGGCTC CTGTAGGCAG CACGGACTTG	60
AACAACCAGA CTCCTGTAGA CGTGTTCAG AACTTACGGA AGCACCCACG ATG GAC	116
Met Asp	
1	
CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG	164
Pro Arg Cys 5 Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu	
10 15	
CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG	212
Leu Ile 20 Ser Asp Ala Val Ser 25 Val Glu Thr Gln Ala Tyr Phe Asn Gly	
30	
ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG	260
Thr Ala Tyr Leu Pro Cys 40 Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu 50	
35 45	
AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC	308
Ser Glu Leu Val 55 Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr 65	
60 65	

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GAG Glu	CAC His	TAT Tyr	TTG Leu 70	GGC Gly	ACA Thr	GAG Glu	AAA Lys 75	CTT Leu 75	GAT Asp	AGT Ser	GTG Val	AAT Asn	GCC Ala 80	AAG Lys	TAC Tyr	356
CTG Leu	GGC Gly	CGC Arg 85	ACG Thr	AGC Ser	TTT Phe	GAC Asp	AGG Arg 90	AAC Asn	AAC Asn	TGG Trp	ACT Thr	CTA Leu 95	CGA Arg	CTT Leu	CAC His	404
AAT Asn 100	GTT Val	CAG Gln	ATC Ile	AAG Lys	GAC Asp	ATG Met 105	GGC Gly	TCG Ser	TAT Tyr	GAT Asp	TGT Cys 110	TTT Phe	ATA Ile	CAA Gln	AAA Lys	452
AAG Lys 115	CCA Pro	CCC Pro	ACA Thr	GGA Gly	TCA Ile 120	ATT Ile	ATC Ile	CTC Leu	CAA Gln	CAG Gln 125	ACA Thr	TTA Leu	ACA Thr	GAA Glu	CTG Leu 130	500
TCA Ser	GTG Val	ATC Ile	GCC Ala	AAC Asn 135	TTC Phe	AGT Ser	GAA Glu	CCT Pro	GAA Glu 140	ATA Ile	AAA Lys	CTG Leu	GCT Ala	CAG Gln 145	AAT Asn	548
GTA Val	ACA Thr	GGA Gly	AAT Asn 150	TCT Ser	GGC Gly	ATA Ile	AAT Asn	TTG Leu 155	ACC Cys	TGC Thr	ACG Thr	TCT Ser	AAG Lys 160	CAA Gln	GGT Gly	596
CAC His	CCG Pro	AAA Lys 165	CCT Pro	AAG Lys	AAG Lys	ATG Met	TAT Tyr 170	TTT Phe	CTG Leu	ATA Ile	ACT Thr	AAT Asn 175	TCA Ser	ACT Thr	AAT Asn	644
GAG Glu 180	TAT Tyr	GGT Gly	GAT Asp	AAC Asn	ATG Met	CAG Gln 185	ATA Ile	TCA Ser	CAA Gln	GAT Asp	AAT Asn 190	GTC Val	ACA Thr	GAA Glu	CTG Leu	692
TTC Phe 195	AGT Ser	ATC Ile	TCC Ser	AAC Asn	AGC Ser 200	CTC Leu	TCT Ser	CTT Leu	TCA Ser	TTC Phe 205	CCG Pro	GAT Asp	GGT Gly	GTG Val	TGG Trp 210	740
CAT His	ATG Met	ACC Thr	GTT Val	GTG Val 215	TGT Cys	GTT Val	CTG Leu	GAA Glu	ACG Thr 220	GAG Glu	TCA Ser	ATG Met	AAG Lys	ATT Ile 225	TCC Ser	788
TCC Ser	AAA Lys	CCT Pro	CTC Leu 230	AAT Asn	TTC Phe	ACT Thr	CAA Gln	GAG Glu 235	TTT Phe	CCA Pro	TCT Ser	CCT Pro	CAA Gln 240	ACG Thr	TAT Tyr	836
TGG Trp	AAG Lys	GAG Glu 245	ATT Ile	ACA Thr	GCT Ala	TCA Ser	GTT Val 250	ACT Thr	GTG Val	GCC Ala	CTC Leu	CTC Leu 255	CTT Leu	GTG Val	ATG Met	884
CTG Leu 260	CTC Leu	ATC Ile	ATT Ile	GTA Val	TGT Cys	CAC His 265	AAG Lys	AAG Lys	CCG Pro	AAT Asn	CAG Gln 270	CCT Pro	AGC Ser	AGG Arg	CCC Pro	932
AGC Ser 275	AAC Asn	ACA Thr	GCC Ala	TCT Ser	AAG Lys 280	TTA Leu	GAG Glu	CGG Arg	GAT Asp 285	AGT Ser	AAC Asn	GCT Ala	GAC Asp	AGA Arg	GAG Glu 290	980
ACT Thr	ATC Ile	AAC Asn	CTG Leu	AAG Lys 295	GAA Glu	CTT Leu	GAA Glu	CCC Pro	CAA Gln 300	ATT Ile	GCT Ala	TCA Ser	GCA Ala	AAA Lys 305	CCA Pro	1028
AAT Asn	GCA Ala	GAG Glu	TGAAGGCAGT	GAGAGCCTGA	GGAAAGAGTT	AAAAATTGCT										1077

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TTGCCTGAAA	TAAGAAGTGC	AGAGTTTCTC	AGAATTCAAA	AATGTTCTCA	GCTGATTGGA	1137
ATTCTACAGT	TGAATAATTA	AAGAAC				1163